



PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

Boo

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Limits

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Show:

☐ 1: LNHUP1. pulmonary surfactant...[gi:71969]

BLink, Domains, Links

LOCUS LNHUP1 248 aa linear PRI 16-JUL-1999
 DEFINITION pulmonary surfactant protein A precursor (clone 1A) - human.
 ACCESSION LNHUP1
 VERSION LNHUP1 GI:71969
 DBSOURCE pir: locus LNHUP1;

summary: #length 248 #molecular-weight 26209 #checksum 4335
 ;
 genetic: #gene GDB:SFTPA1; SFTP1; SP-A; SP-A1 ##cross-references
 GDB:119593; OMIM:178630 #map_position 10q22-10q23
 ;
 superfamily: mannose-binding lectin; C-type lectin homology
 ;
 PIR dates: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change
 16-Jul-1999

KEYWORDS acetylated amino end; alveolar proteinosis; calcium; gaseous
 exchange; glycoprotein; hydroxyproline; lung; pulmonary surfactant;
 respiratory distress syndrome.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 248)

AUTHORS Floros,J., Steinbrink,R., Jacobs,K., Phelps,D., Kriz,R., Recny,M.,
 Sultzman,L., Jones,S., Taeusch,H.W., Frank,H.A. and Fritsch,E.F.

TITLE Isolation and characterization of cDNA clones for the 35-kDa
 pulmonary surfactant-associated protein

JOURNAL J. Biol. Chem. 261 (19), 9029-9033 (1986)

MEDLINE 86250832

PUBMED 3755136

FEATURES

Location/Qualifiers

source

1..248

/organism="Homo sapiens"

/db_xref="taxon:9606"

Protein

1..248

/product="pulmonary surfactant protein A precursor (clone
 1A)"

/note="pulmonary surfactant 32K apoprotein; pulmonary
 surfactant-associated protein PSP-A"

Region

1..20

/region_name="domain"

/note="signal sequence"

Region

21..248

/region_name="product"

/note="pulmonary surfactant protein A"

Site

21

Site /site_type="modified"
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/region_name="domain"
/note="C-type lectin homology #label LCH"
Site 207
/site_type="binding"
/note="carbohydrate (Asn) (covalent)"

ORIGIN

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121 trgalslqgs imtvgekvfs sngqsitfda iqeacaragg riavprnpee neaiasfvkk
181 yntyayvglt egpspgdfry sdgtpvnytn wyrgepagrg keqcvemytd gqwndrnclly
241 srlticef

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